

NOV 05 2001

RECEIVED #8

TECH CENTER 1600/2000

5.11m
 RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/597,732

DATE: 10/30/2001
 TIME: 16:54:41

Input Set : N:\Crf3\RULE60\09597732.txt
 Output Set: N:\CRF3\10302001\I597732.raw

3 <110> APPLICANT: Keating, Mark T.
 4 Sanguinetti, Michael C.
 5 Curran, Mark E.
 6 Landes, Gregory M.
 7 Connors, Timothy D.
 8 Burn, Timothy C.
 9 Splawski, Igor
 11 <120> TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
 13 <130> FILE REFERENCE: 2323-133
 15 <140> CURRENT APPLICATION NUMBER: 09/597,732
 16 <141> CURRENT FILING DATE: 2000-06-19
 18 <150> PRIOR APPLICATION NUMBER: 09/135,010
 19 <151> PRIOR FILING DATE: 1998-08-17
 21 <150> PRIOR APPLICATION NUMBER: 60/094,477
 22 <151> PRIOR FILING DATE: 1998-07-29
 24 <150> PRIOR APPLICATION NUMBER: 08/921,068
 25 <151> PRIOR FILING DATE: 1997-08-29
 27 <150> PRIOR APPLICATION NUMBER: 08/739,383
 28 <151> PRIOR FILING DATE: 1996-10-29
 30 <150> PRIOR APPLICATION NUMBER: 60/019,014
 31 <151> PRIOR FILING DATE: 1995-12-22
 33 <160> NUMBER OF SEQ ID NOS: 116
 35 <170> SOFTWARE: PatentIn Ver. 2.0
 37 <210> SEQ ID NO: 1
 38 <211> LENGTH: 3181
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Homo sapiens
 42 <220> FEATURE:
 43 <221> NAME/KEY: CDS
 44 <222> LOCATION: (163)..(2190)
 46 <400> SEQUENCE: 1
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 51 gtgccgcgc tcgggcggc ccccccggcag gccccttcg tt atg gcc gcg gcc 174
 52 Met Ala Ala Ala
 53 1
 55 tcc tcc ccc agg gcc gag agg aag cgc tgg ggt tgg ggc cgc ctg 222
 56 Ser Ser Pro Pro Arg Ala Glu Arg Lys Arg Trp Gly Trp Gly Arg Leu
 57 5 10 15 20
 59 cca ggc gcc cgg cgg ggc agc gcg ggc ctg gcc aag aag tgc ccc ttc 270
 60 Pro Gly Ala Arg Arg Gly Ser Ala Gly Leu Ala Lys Lys Cys Pro Phe
 61 25 30 35
 63 tcg ctg gag ctg gcg gag ggc ggc cgg ggc ggc ggc gtc tac gcg 318
 64 Ser Leu Glu Leu Ala Glu Gly Gly Pro Ala Gly Ala Leu Tyr Ala
 65 40 45 50
 67 ccc atc gcg ccc ggc gcc cca ggt ccc gcg ccc cct gcg tcc ccg gcc 366
 68 Pro Ile Ala Pro Gly Ala Pro Gly Pro Ala Pro Pro Ala Ser Pro Ala

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69	55	60	65														
71	gca	ccc	gcc	gca	gtt	gcc	tcc	gac	ctt	ggc	ccg	ccg	ccg	ccg	414		
72	Ala	Pro	Ala	Ala	Pro	Pro	Val	Ala	Ser	Asp	Leu	Gly	Pro	Arg	Pro	Pro	
73	70						75				80						
75	gtt	agc	cta	gac	ccg	ccg	gtc	tcc	atc	tac	agc	acg	ccg	ccg	gtg	462	
76	Val	Ser	Leu	Asp	Pro	Arg	Val	Ser	Ile	Tyr	Ser	Thr	Arg	Arg	Pro	Val	
77	85						90			95			100				
79	ttt	gca	ccg	acc	cac	gtc	cag	ggc	ccg	gtc	tac	aac	ttc	ctc	gag	cgt	510
80	Leu	Ala	Arg	Thr	His	Val	Gln	Gly	Arg	Val	Tyr	Asn	Phe	Leu	Glu	Arg	
81	84	Pro	Thr	Gly	Trp	Lys	Cys	Phe	Val	Tyr	His	Phe	Ala	Val	Phe	Ile	558
82	85	105					120			125			130				
87	gtt	ctg	gtc	tgc	ctc	atc	ttc	agc	gtg	ctg	tcc	acc	atc	gag	cag	tat	606
88	Val	Leu	Val	Cys	Leu	Ile	Phe	Ser	Val	Leu	Ser	Thr	Ile	Glu	Gln	Tyr	
89	91	135					140			145							
91	gcc	gcc	ctg	gcc	acg	ggg	act	ctc	ttc	tgg	atg	gag	atc	gtg	ctg	gtg	654
92	Ala	Ala	Leu	Ala	Thr	Gly	Thr	Leu	Phe	Trp	Met	Glu	Ile	Val	Leu	Val	
93	93	150					155			160							
95	gtt	ttc	ggg	acg	gag	tac	gtg	gtc	ccg	ctc	tgg	tcc	gcc	ggc	tgc	702	
96	Val	Phe	Gly	Thr	Glu	Tyr	Val	Val	Arg	Leu	Trp	Ser	Ala	Gly	Cys		
97	97	165					170			175			180				
99	ccg	agc	aag	tac	gtg	ggc	ctc	tgg	ggg	ccg	ctg	ttt	gcc	ccg	aag	750	
100	Arg	Ser	Lys	Tyr	Val	Gly	Leu	Trp	Gly	Arg	Leu	Arg	Phe	Ala	Arg	Lys	
101	101	185					190			195							
103	ccc	att	tcc	atc	atc	gac	ctc	atc	gtg	gtc	gtg	gcc	tcc	atg	gtg	gtc	798
104	Pro	Ile	Ser	Ile	Ile	Asp	Leu	Ile	Val	Val	Val	Ala	Ser	Met	Val	Val	
105	105	200					205			210							
107	ctc	tgc	gtg	ggc	tcc	aag	ggg	cag	gtg	ttt	gcc	acg	tgc	gcc	atc	agg	846
108	Leu	Cys	Val	Gly	Ser	Lys	Gly	Gln	Val	Phe	Ala	Thr	Ser	Ala	Ile	Arg	
109	109	215					220			225							
111	ggc	atc	ccg	ttc	ctg	cag	atc	ctg	agg	atg	cta	cac	gtc	gac	ccg	cag	894
112	Gly	Ile	Arg	Phe	Leu	Gln	Ile	Leu	Arg	Met	Leu	His	Val	Asp	Arg	Gln	
113	113	230					235			240							
115	gga	ggc	acc	tgg	agg	ctc	ctg	ggc	tcc	gtg	gtc	ttc	atc	cac	ccg	cag	942
116	Gly	Gly	Thr	Trp	Arg	Leu	Leu	Gly	Ser	Val	Val	Phe	Ile	His	Arg	Gln	
117	117	245					250			255			260				
119	gag	ctg	ata	acc	ctg	tac	atc	ggc	ttc	ctg	ggc	ctc	atc	ttc	tcc	990	
120	Glu	Leu	Ile	Thr	Leu	Tyr	Ile	Gly	Phe	Leu	Gly	Leu	Ile	Phe	Ser		
121	121	265					270			275							
123	tgc	tac	ttt	gtg	tac	ctg	gct	gag	aag	gac	ccg	gtg	aac	gag	tca	ggc	1038
124	Ser	Tyr	Phe	Val	Tyr	Leu	Ala	Glu	Lys	Asp	Ala	Val	Asn	Glu	Ser	Gly	
125	125	280					285			290							
127	ccg	gtg	gag	ttc	ggc	agg	atc	gca	gat	ccg	ctg	tgg	tgg	ggg	gtg	gtc	1086
128	Arg	Val	Glu	Phe	Gly	Ser	Tyr	Ala	Asp	Ala	Leu	Trp	Trp	Gly	Val	Val	
129	129	295					300			305							
131	aca	gtc	acc	acc	atc	ggc	tat	ggg	gac	aag	gtg	ccc	cag	acg	tgg	gtc	1134
132	Thr	Val	Thr	Thr	Ile	Gly	Tyr	Gly	Asp	Lys	Val	Pro	Gln	Thr	Trp	Val	
133	133	310					315			320							

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135	ggg aag acc atc gcc tcc tgc ttc tct gtc ttt gcc atc tcc ttc ttt	1182
136	Gly Lys Thr Ile Ala Ser Cys Phe Ser Val Phe Ala Ile Ser Phe Phe	
137	325 330 335 340	
139	gcg ctc cca gcg ggg att ctt ggc tcg ggg ttt gcc ctg aag gtg cag	1230
140	Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val Gln	
141	345 350 355	
143	cag aag cag agg cag aag cac ttc aac cgg cag atc ccg gcg gca gcc	1278
144	Gln Lys Gln Arg Gln Lys His Phe Asn Arg Gln Ile Pro Ala Ala Ala	
145	360 365 370	
147	tca ctc att cag acc gca tgg agg tgc tat gct gcc gag aac ccc gac	1326
148	Ser Leu Ile Gln Thr Ala Trp Arg Cys Tyr Ala Ala Glu Asn Pro Asp	
149	375 380 385	
151	tcc tcc acc tgg aag atc tac atc cgg aag gcc ccc cgg agc cac act	1374
152	Ser Ser Thr Trp Lys Ile Tyr Ile Arg Lys Ala Pro Arg Ser His Thr	
153	390 395 400	
155	ctg ctg tca ccc agc ccc aaa ccc aag aag tct gtg gtg gta aag aaa	1422
156	Leu Leu Ser Pro Ser Pro Lys Pro Lys Lys Ser Val Val Val Lys Lys	
157	405 410 415 420	
159	aaa aag ttc aag ctg gac aaa gac aat ggg gtg act cct gga gag aag	1470
160	Lys Lys Phe Lys Leu Asp Lys Asp Asn Gly Val Thr Pro Gly Glu Lys	
161	425 430 435	
163	atg ctc aca gtc ccc cat atc acg tgc gac ccc cca gaa gag cgg cgg	1518
164	Met Leu Thr Val Pro His Ile Thr Cys Asp Pro Pro Glu Glu Arg Arg	
165	440 445 450	
167	ctg gac cac ttc tct gtc gac ggc tat gac agt tct gta agg aag agc	1566
168	Leu Asp His Phe Ser Val Asp Gly Tyr Asp Ser Ser Val Arg Lys Ser	
169	455 460 465	
171	cca aca ctg ctg gaa gtg agc atg ccc cat ttc atg aga acc aac agc	1614
172	Pro Thr Leu Leu Glu Val Ser Met Pro His Phe Met Arg Thr Asn Ser	
173	470 475 480	
175	tcc gcc gag gac ctg gac ctg gaa ggg gag act ctg ctg aca ccc atc	1662
176	Phe Ala Glu Asp Leu Asp Leu Glu Gly Glu Thr Leu Leu Thr Pro Ile	
177	485 490 495 500	
179	acc cac atc tca cag ctg cgg gaa cac cat cgg gcc acc att aag gtc	1710
180	Thr His Ile Ser Gln Leu Arg Glu His His Arg Ala Thr Ile Lys Val	
181	505 510 515	
183	att cga cgc atg cag tac ttt gtg gcc aag aag aaa ttc cag caa gcg	1758
184	Ile Arg Arg Met Gln Tyr Phe Val Ala Lys Lys Lys Phe Gln Gln Ala	
185	520 525 530	
187	cgg aag cct tac gat gtg cgg gac gtc att gag cag tac tcg cag ggc	1806
188	Arg Lys Pro Tyr Asp Val Arg Asp Val Ile Glu Gln Tyr Ser Gln Gly	
189	535 540 545	
191	cac ctc aac ctc atg gtg cgc atc aag gag ctg cag agg agg ctg gac	1854
192	His Leu Asn Leu Met Val Arg Ile Lys Glu Leu Gln Arg Arg Leu Asp	
193	550 555 560	
195	cag tcc att ggg aag ccc tca ctg ttc atc tcc gtc tca gaa aag agc	1902
196	Gln Ser Ile Gly Lys Pro Ser Leu Phe Ile Ser Val Ser Glu Lys Ser	
197	565 570 575 580	
199	aag gat cgc ggc agc aac acg atc ggc gcc cgc ctg aac cga gta gaa	1950

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200 Lys Asp Arg Gly Ser Asn Thr Ile Gly Ala Arg Leu Asn Arg Val Glu
201 585 590 595
203 gac aag gtg acg cag ctg gac cag agg ctg gca ctc atc acc gac atg 1998
204 Asp Lys Val Thr Gln Leu Asp Gln Arg Leu Ala Leu Ile Thr Asp Met
205 600 605 610
207 ctt cac cag ctg ctc tcc ttg cac ggt ggc agc acc ccc ggc agc ggc 2046
208 Leu His Gln Leu Leu Ser Leu His Gly Gly Ser Thr Pro Gly Ser Gly
209 615 620 625
211 ggc ccc ccc aga gag ggc ggg gcc cac atc acc cag ccc tgc ggc agt 2094
212 Gly Pro Pro Arg Glu Gly Ala His Ile Thr Gln Pro Cys Gly Ser
213 630 635 640
215 ggc ggc tcc gtc gac cct gag ctc ttc ctg ccc agc aac acc ctg ccc 2142
216 Gly Gly Ser Val Asp Pro Glu Leu Phe Leu Pro Ser Asn Thr Leu Pro
217 645 650 655 660
219 acc tac gag cag ctg acc gtg ccc agg agg ggc ccc gat gag ggg tcc 2190
220 Thr Tyr Glu Gln Leu Thr Val Pro Arg Arg Gly Pro Asp Glu Gly Ser
221 665 670 675
223 tgaggagggg atggggctgg gggatgggcc tgagtgagag gggaggccaa gagtggcccc 2250
225 acctggccct ctctgaagga ggcacactcc taaaaggccc agagagaaga gcccactct 2310
227 cagaggcccc aataccccc atgaccatgt gtctggcaca gcctgcactt gggggctcag 2370
229 caaggccacc tcttcctggc cgggtgtggg gccccgtctc aggtctgagt ttttacccca 2430
231 agcgcctgg ccccccacatg gtgtatgttga catcaactggc atgggtgggt ggacccagtg 2490
233 gcagggcaca gggcctggcc catgtatggc caggaagtag cacaggtgta gtgcaggccc 2550
235 accctgttgc gcccaggggg cttcctgagg ggagacagag caacccctgg accccagcct 2610
237 caaatccagg accctgtccag gcacaggcag ggcaggacca gcccacgtg actacagggc 2670
239 caccggcaat aaaagccca gagccattt ggaggccctg ggcctggctc cctcaactctc 2730
241 agaaaatgtt gaccatggg caggagactg tggagactgc tcctgagccc ccagcttcca 2790
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245 ttccctgggt tagactgcca gctttccata gctggagagg agccctgcct ctccggccct 2910
247 gagcccaactg tgcgtggggc tcccgccctc aacccttcgc ccagtccctgg cagccagcc 2970
249 aacacacaga agggactgc cacccccc tgcacgtgc tgagccgcag agaagtgc 3030
251 gttcctacac aggacagggg ttccctctgg gcattacatc gcatagaaat caataatttgc 3090
253 tggtgatttg gatctgtgtt ttaatgagg tcacagtgtg attttgattt ttaattgtgc 3150
255 aagctttcc taataaacgt ggagaatcac a 3181
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259 <211> LENGTH: 676
260 <212> TYPE: PRT
261 <213> ORGANISM: Homo sapiens
263 <400> SEQUENCE: 2
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265 1 5 10 15
267 Trp Gly Arg Leu Pro Gly Ala Arg Arg Gly Ser Ala Gly Leu Ala Lys
268 20 25 30
270 Lys Cys Pro Phe Ser Leu Glu Leu Ala Glu Gly Gly Pro Ala Gly Gly
271 35 40 45
273 Ala Leu Tyr Ala Pro Ile Ala Pro Gly Ala Pro Gly Pro Ala Pro Pro
274 50 55 60
276 Ala Ser Pro Ala Ala Pro Ala Pro Pro Val Ala Ser Asp Leu Gly
277 65 70 75 80

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279 Pro Arg Pro Pro Val Ser Leu Asp Pro Arg Val Ser Ile Tyr Ser Thr
 280 85 90 95
 282 Arg Arg Pro Val Leu Ala Arg Thr His Val Gln Gly Arg Val Tyr Asn
 283 100 105 110
 285 Phe Leu Glu Arg Pro Thr Gly Trp Lys Cys Phe Val Tyr His Phe Ala
 286 115 120 125
 288 Val Phe Leu Ile Val Leu Val Cys Leu Ile Phe Ser Val Leu Ser Thr
 289 130 135 140
 291 Ile Glu Gln Tyr Ala Ala Leu Ala Thr Gly Thr Leu Phe Trp Met Glu
 292 145 150 155 160
 294 Ile Val Leu Val Val Phe Phe Gly Thr Glu Tyr Val Val Arg Leu Trp
 295 165 170 175
 297 Ser Ala Gly Cys Arg Ser Lys Tyr Val Gly Leu Trp Gly Arg Leu Arg
 298 180 185 190
 300 Phe Ala Arg Lys Pro Ile Ser Ile Ile Asp Leu Ile Val Val Val Ala
 301 195 200 205
 303 Ser Met Val Val Leu Cys Val Gly Ser Lys Gly Gln Val Phe Ala Thr
 304 210 215 220
 306 Ser Ala Ile Arg Gly Ile Arg Phe Leu Gln Ile Leu Arg Met Leu His
 307 225 230 235 240
 309 Val Asp Arg Gln Gly Gly Thr Trp Arg Leu Leu Gly Ser Val Val Phe
 310 245 250 255
 312 Ile His Arg Gln Glu Leu Ile Thr Thr Leu Tyr Ile Gly Phe Leu Gly
 313 260 265 270
 315 Leu Ile Phe Ser Ser Tyr Phe Val Tyr Leu Ala Glu Lys Asp Ala Val
 316 275 280 285
 318 Asn Glu Ser Gly Arg Val Glu Phe Gly Ser Tyr Ala Asp Ala Leu Trp
 319 290 295 300
 321 Trp Gly Val Val Thr Val Thr Ile Gly Tyr Gly Asp Lys Val Pro
 322 305 310 315 320
 324 Gln Thr Trp Val Gly Lys Thr Ile Ala Ser Cys Phe Ser Val Phe Ala
 325 325 330 335
 327 Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala
 328 340 345 350
 330 Leu Lys Val Gln Gln Lys Gln Arg Gln Lys His Phe Asn Arg Gln Ile
 331 355 360 365
 333 Pro Ala Ala Ala Ser Leu Ile Gln Thr Ala Trp Arg Cys Tyr Ala Ala
 334 370 375 380
 336 Glu Asn Pro Asp Ser Ser Thr Trp Lys Ile Tyr Ile Arg Lys Ala Pro
 337 385 390 395 400
 339 Arg Ser His Thr Leu Leu Ser Pro Ser Pro Lys Pro Lys Lys Ser Val
 340 405 410 415
 342 Val Val Lys Lys Lys Phe Lys Leu Asp Lys Asp Asn Gly Val Thr
 343 420 425 430
 345 Pro Gly Glu Lys Met Leu Thr Val Pro His Ile Thr Cys Asp Pro Pro
 346 435 440 445
 348 Glu Glu Arg Arg Leu Asp His Phe Ser Val Asp Gly Tyr Asp Ser Ser
 349 450 455 460
 351 Val Arg Lys Ser Pro Thr Leu Leu Glu Val Ser Met Pro His Phe Met

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09597732.txt
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L:442 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:445 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:447 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3